

RECEIVED

SEQUENCE LISTING

APR 1 2 2002

TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Jaye, Michael C.
Lynch, Kevin J.
Amin, Dilip V.
Doan, Kim-Anh T.
Marchadier, Dawn
Maugeais, Cyrille
Rader, Daniel J.
Krawiec, John A.
South, Victoria J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE
LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND
APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN
(VLDL) CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL) CHOLESTEROL

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Synnestvedt & Lechner LLP
(B) STREET: Suite 2600 Aramark Tower, 1101 Market Street
(C) CITY: Philadelphia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19107

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-Windows 95
(D) SOFTWARE: Corel WordPerfect 8.0 converted to ASCII

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/277,401
(B) FILING DATE: March 26, 1999
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kelly, Ph.D., Patrick J.
(B) REGISTRATION NUMBER: 34,638
(C) REFERENCE/DOCKET NUMBER: 22,944-C USA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 923-4466
(B) TELEFAX: (215) 923-2189

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

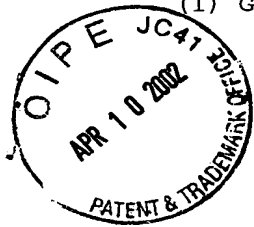
(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 22..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCT TGATCAATCG C TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC .51
Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg
1 5 10
AAG AAC CGT TGT AAT AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC 99
Lys Asn Arg Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn
15 20 25



7'

AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC 147
 Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe
 30 35 40
 AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC 200
 Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro
 45 50
 TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA 260
 TCCAATCAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA 320
 CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC 367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser
 1 5 10 15
 Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met
 20 25 30
 Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser
 35 40 45
 Leu Glu Cys Pro
 50

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 312..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGGG GGGGGGGGGG 60
 TCAGCGAGTC CTTGCCTCCC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC 120
 CGTTGACACT CGCTCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC 180
 CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG 240
 CTGGAAACAC CAAGAGGTGG TTTTGTGTTT TTAAACTTC TGTTTCTTGG GAGGGGGTGT 300
 GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC 350
 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu
 1 5 10
 TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA 398
 Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly
 15 20 25
 CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC 446
 Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val
 30 35 40 45
 AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT 494
 Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His
 50 55 60
 GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC 542
 Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys
 65 70 75
 AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG 590
 Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr
 80 85 90

71
cont.

ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG 638
 Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu
 95 100 105
 CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC 686
 His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro
 110 115 120 125
 CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG 734
 Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val
 130 135 140
 GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT 782
 Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp
 145 150 155
 TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC 830
 Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His
 160 165 170
 GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC 878
 Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile
 175 180 185
 ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC 926
 Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His
 190 195 200 205
 AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC 974
 Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr
 210 215 220
 TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC 1022
 Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly
 225 230 235
 CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA 1070
 His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly
 240 245 250
 CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG 1118
 Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val
 255 260 265
 GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG 1166
 Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
 270 275 280 285
 GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT 1214
 Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
 290 295 300
 CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT 1262
 Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
 305 310 315
 AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA 1310
 Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
 320 325 330
 ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG 1358
 Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln
 335 340 345
 TCC CTG GAG TGT CAAGCCGAAT TC 1382
 Ser Leu Glu Cys
 350

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1 5 10 15

Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
 20 25 30
 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
 35 40 45
 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
 50 55 60
 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
 65 70 75 80
 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
 85 90 95
 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
 100 105 110
 Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
 115 120 125
 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
 130 135 140
 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
 145 150 155 160
 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
 165 170 175
 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
 180 185 190
 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
 195 200 205
 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
 210 215 220
 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
 225 230 235 240
 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
 245 250 255
 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
 260 265 270
 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
 275 280 285
 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
 290 295 300
 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
 305 310 315 320
 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
 325 330 335
 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
 340 345 350
 Cys

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC
 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1 5 10 15

48

TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA

96

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Phe | Ala | Ala | Gly | Ser | Pro | Val | Pro | Phe | Gly | Pro | Glu | Gly | Arg | Leu | Glu | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| GAT | AAG | CTC | CAC | AAA | CCC | AAA | GCT | ACA | CAG | ACT | GAG | GTC | AAA | CCA | TCT | 144 | |
| Asp | Lys | Leu | His | Lys | Pro | Lys | Ala | Thr | Gln | Thr | Glu | Val | Lys | Pro | Ser | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| GTG | AGG | TTT | AAC | CTC | CGC | ACC | TCC | AAG | GAC | CCA | GAG | CAT | GAA | GGA | TGC | 192 | |
| Val | Arg | Phe | Asn | Leu | Arg | Thr | Ser | Lys | Asp | Pro | Glu | His | Glu | Gly | Cys | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | |
| TAC | CTC | TCC | GTC | GGC | CAC | AGC | CAG | CCC | TTA | GAA | GAC | TGC | AGT | TTC | AAC | 240 | |
| Tyr | Leu | Ser | Val | Gly | His | Ser | Gln | Pro | Leu | Glu | Asp | Cys | Ser | Phe | Asn | | |
| | | 65 | | | 70 | | | | | 75 | | | | | 80 | | |
| ATG | ACA | GCT | AAA | ACC | TTT | TTC | ATC | ATT | CAC | GGA | TGG | ACG | ATG | AGC | GGT | 288 | |
| Met | Thr | Ala | Lys | Thr | Phe | Phe | Ile | Ile | His | Gly | Trp | Thr | Met | Ser | Gly | | |
| | | | 85 | | | | | | 90 | | | | | 95 | | | |
| ATC | TTT | GAA | AAC | TGG | CTG | CAC | AAA | CTC | GTG | TCA | GCC | CTG | CAC | ACA | AGA | 336 | |
| Ile | Phe | Glu | Asn | Trp | Leu | His | Lys | Leu | Val | Ser | Ala | Leu | His | Thr | Arg | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | |
| GAG | AAA | GAC | GCC | AAT | GTA | GTT | GTG | GTT | GAC | TGG | CTC | CCC | CTG | GCC | CAC | 384 | |
| Glu | Lys | Asp | Ala | Asn | Val | Val | Val | Val | Asp | Trp | Leu | Pro | Leu | Ala | His | | |
| | | 115 | | | | | 120 | | | | | | 125 | | | | |
| CAG | CTT | TAC | ACG | GAT | GCG | GTC | AAT | AAT | ACC | AGG | GTG | GTG | GGA | CAC | AGC | 432 | |
| Gln | Leu | Tyr | Thr | Asp | Ala | Val | Asn | Asn | Thr | Arg | Val | Val | Gly | His | Ser | | |
| | | 130 | | | | 135 | | | | | | | 140 | | | | |
| ATT | GCC | AGG | ATG | CTC | GAC | TGG | CTG | CAG | GAG | AAG | GAC | GAT | TTT | TCT | CTC | 480 | |
| Ile | Ala | Arg | Met | Leu | Asp | Trp | Leu | Gln | Glu | Lys | Asp | Asp | Phe | Ser | Leu | | |
| | | 145 | | | 150 | | | | | 155 | | | | | 160 | | |
| GGG | AAT | GTC | CAC | TTG | ATC | GGC | TAC | AGC | CTC | GGA | GCG | CAC | GTG | GCC | GGG | 528 | |
| Gly | Asn | Val | His | Leu | Ile | Gly | Tyr | Ser | Leu | Gly | Ala | His | Val | Ala | Gly | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| TAT | GCA | GGC | AAC | TTC | GTG | AAA | GGA | ACG | GTG | GGC | CGA | ATC | ACA | GGT | TTG | 576 | |
| Tyr | Ala | Gly | Asn | Phe | Val | Lys | Gly | Thr | Val | Gly | Arg | Ile | Thr | Gly | Leu | | |
| | | | 180 | | | | 185 | | | | | | | 190 | | | |
| GAT | CCT | GCC | GGG | CCC | ATG | TTT | GAA | GGG | GCC | GAC | ATC | CAC | AAG | AGG | CTC | 624 | |
| Asp | Pro | Ala | Gly | Pro | Met | Phe | Glu | Gly | Ala | Asp | Ile | His | Lys | Arg | Leu | | |
| | | 195 | | | | | 200 | | | | | | 205 | | | | |
| TCT | CCG | GAC | GAT | GCA | GAT | TTT | GTG | GAT | GTC | CTC | CAC | ACC | TAC | ACG | CGT | 672 | |
| Ser | Pro | Asp | Asp | Ala | Asp | Phe | Val | Asp | Val | Leu | His | Thr | Tyr | Thr | Arg | | |
| | | 210 | | | | 215 | | | | | | | 220 | | | | |
| TCC | TTC | GGC | TTG | AGC | ATT | GGT | ATT | CAG | ATG | CCT | GTG | GGC | CAC | ATT | GAC | 720 | |
| Ser | Phe | Gly | Leu | Ser | Ile | Gly | Ile | Gln | Met | Pro | Val | Gly | His | Ile | Asp | | |
| | | | | | 230 | | | | | 235 | | | | | 240 | | |
| ATC | TAC | CCC | AAT | GGG | GGT | GAC | TTC | CAG | CCA | GGC | TGT | GGA | CTC | AAC | GAT | 768 | |
| Ile | Tyr | Pro | Asn | Gly | Gly | Asp | Phe | Gln | Pro | Gly | Cys | Gly | Leu | Asn | Asp | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| GTC | TTG | GGA | TCA | ATT | GCA | TAT | GGA | ACA | ATC | ACA | GAG | GTG | GTA | AAA | TGT | 816 | |
| Val | Leu | Gly | Ser | Ile | Ala | Tyr | Gly | Thr | Ile | Thr | Glu | Val | Val | Lys | Cys | | |
| | | | 260 | | | | | 265 | | | | | | 270 | | | |
| GAG | CAT | GAG | CGA | GCC | GTC | CAC | CTC | TTT | GTT | GAC | TCT | CTG | GTG | AAT | CAG | 864 | |
| Glu | His | Glu | Arg | Ala | Val | His | Leu | Phe | Val | Asp | Ser | Leu | Val | Asn | Gln | | |
| | | 275 | | | | | 280 | | | | | | | 285 | | | |
| GAC | AAG | CCG | AGT | TTT | GCC | TTC | CAG | TGC | ACT | GAC | TCC | AAT | CGC | TTC | AAA | 912 | |
| Asp | Lys | Pro | Ser | Phe | Ala | Phe | Gln | Cys | Thr | Asp | Ser | Asn | Arg | Phe | Lys | | |
| | | 290 | | | | 295 | | | | | | | 300 | | | | |
| AAG | GGG | ATC | TGT | CTG | AGC | TGC | CGC | AAG | AAC | CGT | TGT | AAT | AGC | ATT | GGC | 960 | |
| Lys | Gly | Ile | Cys | Leu | Ser | Cys | Arg | Lys | Asn | Arg | Cys | Asn | Ser | Ile | Gly | | |
| | | 305 | | | 310 | | | | | 315 | | | | | 320 | | |
| TAC | AAT | GCC | AAG | AAA | ATG | AGG | AAC | AAG | AGG | AAC | AGC | AAA | ATG | TAC | CTA | 1008 | |
| Tyr | Asn | Ala | Lys | Lys | Met | Arg | Asn | Lys | Arg | Asn | Ser | Lys | Met | Tyr | Leu | | |
| | | | | 325 | | | | | 330 | | | | | | 335 | | |
| AAA | ACC | CGG | GCA | GGC | ATG | CCT | TTC | AGA | GGT | AAC | CTT | CAG | TCC | CTG | GAG | 1056 | |

7'
cont.

Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
 340 345 350
 TGT CCC TGA
 Cys Pro

1065

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1 5 10 15
 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
 20 25 30
 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
 35 40 45
 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
 50 55 60
 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
 65 70 75 80
 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
 85 90 95
 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
 100 105 110
 Glu Lys Asp Ala Asn Val Val Val Asp Trp Leu Pro Leu Ala His
 115 120 125
 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
 130 135 140
 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
 145 150 155 160
 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
 165 170 175
 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
 180 185 190
 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
 195 200 205
 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
 210 215 220
 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
 225 230 235 240
 Ile Tyr Pro Asn Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
 245 250 255
 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
 260 265 270
 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
 275 280 285
 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
 290 295 300
 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
 305 310 315 320
 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
 325 330 335
 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
 340 345 350
 Cys Pro

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2565 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 252..1754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|---|---|------------|------------|------------|------------|-----|
| GAATTCGCGG | CCGCGTCGAC | GGCGGCTCAG | GACGAGGGCA | GATCTCGTTC | TGGGGCAAGC | 60 |
| CGTTGACACT | CGCTCCCTGC | CACCGCCCGG | GCTCCGTGCC | GCCAAGTTTT | CATTTTCCAC | 120 |
| CTTCTCTGCC | TCCAGTCCCC | CAGCCCCTGG | CCGAGAGAAG | GGTCTTACCG | GCCGGGATTG | 180 |
| CTGGAAACAC | CAAGAGGTGG | TTTTTGTTTT | TTAAAACTTC | TGTTTCTTGG | GAGGGGGTGT | 240 |
| GGCGGGGCAG | G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC | 290 | | | | |
| | Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu | | | | | |
| | 1 5 10 | | | | | |
| TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA | 338 | | | | | |
| Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly | | | | | | |
| 15 20 25 | | | | | | |
| CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC | 386 | | | | | |
| Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val | | | | | | |
| 30 35 40 45 | | | | | | |
| AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT | 434 | | | | | |
| Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His | | | | | | |
| 50 55 60 | | | | | | |
| GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC | 482 | | | | | |
| Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys | | | | | | |
| 65 70 75 | | | | | | |
| AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG | 530 | | | | | |
| Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr | | | | | | |
| 80 85 90 | | | | | | |
| ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG | 578 | | | | | |
| Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu | | | | | | |
| 95 100 105 | | | | | | |
| CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC | 626 | | | | | |
| His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro | | | | | | |
| 110 115 120 125 | | | | | | |
| CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG | 674 | | | | | |
| Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val | | | | | | |
| 130 135 140 | | | | | | |
| GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT | 722 | | | | | |
| Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp | | | | | | |
| 145 150 155 | | | | | | |
| TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC | 770 | | | | | |
| Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His | | | | | | |
| 160 165 170 | | | | | | |
| GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC | 818 | | | | | |
| Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile | | | | | | |
| 175 180 185 | | | | | | |
| ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC | 866 | | | | | |
| Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His | | | | | | |
| 190 195 200 205 | | | | | | |
| AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC | 914 | | | | | |
| Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr | | | | | | |
| 210 215 220 | | | | | | |
| TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC | 962 | | | | | |
| Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly | | | | | | |
| 225 230 235 | | | | | | |
| CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA | 1010 | | | | | |

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cont.

| | | | | | | | | | | | | | | | | | |
|-------------|-------------|------------|------------|------------|-------------|-----|-----|-------|-------|------------|------------|-----|-----|-----|-----|------|--|
| His | Ile | Asp | Ile | Tyr | Pro | Asn | Gly | Gly | Asp | Phe | Gln | Pro | Gly | Cys | Gly | | |
| | | 240 | | | | | 245 | | | | 250 | | | | | | |
| CTC | AAC | GAT | GTC | TTG | GGA | TCA | ATT | GCA | TAT | GGA | ACA | ATC | ACA | GAG | GTG | 1058 | |
| Leu | Asn | Asp | Val | Leu | Gly | Ser | Ile | Ala | Tyr | Gly | Thr | Ile | Thr | Glu | Val | | |
| | | 255 | | | | | 260 | | | | 265 | | | | | | |
| GTA | AAA | TGT | GAG | CAT | GAG | CGA | GCC | GTC | CAC | CTC | TTT | GTT | GAC | TCT | CTG | 1106 | |
| Val | Lys | Cys | Glu | His | Glu | Arg | Ala | Val | His | Leu | Phe | Val | Asp | Ser | Leu | | |
| | | 270 | | | | | 275 | | | | 280 | | | | 285 | | |
| GTG | AAT | CAG | GAC | AAG | CCG | AGT | TTT | GCC | TTC | CAG | TGC | ACT | GAC | TCC | AAT | 1154 | |
| Val | Asn | Gln | Asp | Lys | Pro | Ser | Phe | Ala | Phe | Gln | Cys | Thr | Asp | Ser | Asn | | |
| | | | | 290 | | | | | | 295 | | | | 300 | | | |
| CGC | TTC | AAA | AAG | GGG | ATC | TGT | CTG | AGC | TGC | CGC | AAG | AAC | CGT | TGT | AAT | 1202 | |
| Arg | Phe | Lys | Lys | Gly | Ile | Cys | Leu | Ser | Cys | Arg | Lys | Asn | Arg | Cys | Asn | | |
| | | | 305 | | | | | | | 310 | | | | 315 | | | |
| AGC | ATT | GGC | TAC | AAT | GCC | AAG | AAA | ATG | AGG | AAC | AAG | AGG | AAC | AGC | AAA | 1250 | |
| Ser | Ile | Gly | Tyr | Asn | Ala | Lys | Lys | Met | Arg | Asn | Lys | Arg | Asn | Ser | Lys | | |
| | | 320 | | | | | | | | 325 | | | | 330 | | | |
| ATG | TAC | CTA | AAA | ACC | CGG | GCA | GGC | ATG | CCT | TTC | AGA | GTT | TAC | CAT | TAT | 1298 | |
| Met | Tyr | Leu | Lys | Thr | Arg | Ala | Gly | Met | Pro | Phe | Arg | Val | Tyr | His | Tyr | | |
| | | 335 | | | | | | | | 340 | | | | 345 | | | |
| CAG | ATG | AAA | ATC | CAT | GTC | TTC | AGT | TAC | AAG | AAC | ATG | GGA | GAA | ATT | GAG | 1346 | |
| Gln | Met | Lys | Ile | His | Val | Phe | Ser | Tyr | Lys | Asn | Met | Gly | Glu | Ile | Glu | | |
| | | 350 | | | | | | | | 355 | | | | 360 | | | |
| CCC | ACC | TTT | TAC | GTC | ACC | CTT | TAT | GGC | ACT | AAT | GCA | GAT | TCC | CAG | ACT | 1394 | |
| Pro | Thr | Phe | Tyr | Val | Thr | Leu | Tyr | Gly | Thr | Asn | Ala | Asp | Ser | Gln | Thr | | |
| | | | | 370 | | | | | | 375 | | | | 380 | | | |
| CTG | CCA | CTG | GAA | ATA | GTG | GAG | CGG | ATC | GAG | CAG | AAT | GCC | ACC | AAC | ACC | 1442 | |
| Leu | Pro | Leu | Glu | Ile | Val | Glu | Arg | Ile | Glu | Gln | Asn | Ala | Thr | Asn | Thr | | |
| | | | 385 | | | | | | | 390 | | | | 395 | | | |
| TTC | CTG | GTC | TAC | ACC | GAG | GAG | GAC | TTG | GGA | GAC | CTC | TTG | AAG | ATC | CAG | 1490 | |
| Phe | Leu | Val | Tyr | Thr | Glu | Glu | Asp | Leu | Gly | Asp | Leu | Leu | Lys | Ile | Gln | | |
| | | 400 | | | | | | | | 405 | | | | 410 | | | |
| CTC | ACC | TGG | GAG | GGG | GCC | TCT | CAG | TCT | TGG | TAC | AAC | CTG | TGG | AAG | GAG | 1538 | |
| Leu | Thr | Trp | Glu | Gly | Ala | Ser | Gln | Ser | Trp | Tyr | Asn | Leu | Trp | Lys | Glu | | |
| | | 415 | | | | | | | | 420 | | | | 425 | | | |
| TTT | CGC | AGC | TAC | CTG | TCT | CAA | CCC | CGC | AAC | CCC | GGA | CGG | GAG | CTG | AAT | 1586 | |
| Phe | Arg | Ser | Tyr | Leu | Ser | Gln | Pro | Arg | Asn | Pro | Gly | Arg | Glu | Leu | Asn | | |
| | | 430 | | | | | | | | 435 | | | | 440 | | | |
| ATC | AGG | CGC | ATC | CGG | GTG | AAG | TCT | GGG | GAA | ACC | CAG | CGG | AAA | CTG | ACA | 1634 | |
| Ile | Arg | Arg | Ile | Arg | Val | Lys | Ser | Gly | Glu | Thr | Gln | Arg | Lys | Leu | Thr | | |
| | | | | 450 | | | | | | 455 | | | | 460 | | | |
| TTT | TGT | ACA | GAA | GAC | CCT | GAG | AAC | ACC | AGC | ATA | TCC | CCA | GGC | CGG | GAG | 1682 | |
| Phe | Cys | Thr | Glu | Asp | Pro | Glu | Asn | Thr | Ser | Ile | Ser | Pro | Gly | Arg | Glu | | |
| | | 465 | | | | | | | | 470 | | | | 475 | | | |
| CTC | TGG | TTT | CGC | AAG | TGT | CGG | GAT | GGC | TGG | AGG | ATG | AAA | AAC | GAA | ACC | 1730 | |
| Leu | Trp | Phe | Arg | Lys | Cys | Arg | Asp | Gly | Trp | Arg | Met | Lys | Asn | Glu | Thr | | |
| | | 480 | | | | | | | | 485 | | | | 490 | | | |
| AGT | CCC | ACT | GTG | GAG | CTT | CCC | TGA | GGGTG | CCCGG | GCAAGTCTTG | CCAGCAAGGC | | | | | 1784 | |
| Ser | Pro | Thr | Val | Glu | Leu | Pro | | | | | | | | | | | |
| | | 495 | | | | | 500 | | | | | | | | | | |
| AGCAAGACTT | CCTGCTATCC | AAGCCCATGG | AGGAAAGTTA | CTGCTGAGGA | CCCACCCAAT | | | | | | | | | | | 1844 | |
| GGAAGGATTG | TTCTCAGCCT | TGACCCTGGA | GCACTGGGAA | CAACTGGTCT | CCTGTGATGG | | | | | | | | | | | 1904 | |
| CTGGGACTCC | TCGCGGGAGG | GGACTGCGCT | GCTATAGCTC | TTGCTGCCTC | TCTTGAATAG | | | | | | | | | | | 1964 | |
| CTCTAACTCC | AAACCTCTGT | CCACACCTCC | AGAGCACCAA | GTCCAGATTT | GTGTGTAAGC | | | | | | | | | | | 2024 | |
| AGCTGGGTGC | CTGGGGCCTC | TCGTGCACAC | TGGATTGGTT | TCTCAGTTGC | TGGGCGAGCC | | | | | | | | | | | 2084 | |
| TGTACTCTGC | CTGACGAGGA | ACGCTGGCTC | CGAAGAGGCC | CTGTGTAGAA | GGCTGTGTCAG | | | | | | | | | | | 2144 | |
| TGCTCAGCCT | GCTTTGAGCC | TCAGTGAGAA | GTCCTTCCGA | CAGGAGCTGA | CTCATGTCAG | | | | | | | | | | | 2204 | |
| GATGGCAGGC | CTGGTATCTT | GCTCGGGCCC | TGGCTGTTGG | GGTTCTCATG | GGTTGCACTG | | | | | | | | | | | 2264 | |
| ACCATACTGC | TTACGTCTTA | GCCATTCCGT | CCTGCTCCCC | AGCTCACTCT | CTGAAGCACA | | | | | | | | | | | 2324 | |
| CATCATTTGGC | TTTCTATTTT | TTCTGTTCAT | TTTTTAATTG | AGCAAATGTC | TATTGAACAC | | | | | | | | | | | 2384 | |
| TTAAAATTAA | TTAGAAATGTG | GTAATGGACA | TATTACTGAG | CCTCTCCATT | TGGAACCCAG | | | | | | | | | | | 2444 | |

7' cont.

| | |
|---|------|
| TGGAGTTGGG ATTTCTAGAC CCTCTTTCTG TTTGGATGGT GTATGTGTAT ATGCATGGGG | 2504 |
| AAAGGCACCT GGGGCCTGGG GGAGGCTATA GGATATAAGC AGTCGACGCG GCCGCGAATT | 2564 |
| C | 2565 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

7'
cont.

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Ser | Val | Pro | Leu | Leu | Cys | Phe | Trp | Ser | Leu | Cys | Tyr | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Ala | Ala | Gly | Ser | Pro | Val | Pro | Phe | Gly | Pro | Glu | Gly | Arg | Leu | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asp | Lys | Leu | His | Lys | Pro | Lys | Ala | Thr | Gln | Thr | Glu | Val | Lys | Pro | Ser |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Val | Arg | Phe | Asn | Leu | Arg | Thr | Ser | Lys | Asp | Pro | Glu | His | Glu | Gly | Cys |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Tyr | Leu | Ser | Val | Gly | His | Ser | Gln | Pro | Leu | Glu | Asp | Cys | Ser | Phe | Asn |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Met | Thr | Ala | Lys | Thr | Phe | Phe | Ile | Ile | His | Gly | Trp | Thr | Met | Ser | Gly |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ile | Phe | Glu | Asn | Trp | Leu | His | Lys | Leu | Val | Ser | Ala | Leu | His | Thr | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Lys | Asp | Ala | Asn | Val | Val | Val | Val | Asp | Trp | Leu | Pro | Leu | Ala | His |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Leu | Tyr | Thr | Asp | Ala | Val | Asn | Asn | Thr | Arg | Val | Val | Gly | His | Ser |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ile | Ala | Arg | Met | Leu | Asp | Trp | Leu | Gln | Glu | Lys | Asp | Asp | Phe | Ser | Leu |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Gly | Asn | Val | His | Leu | Ile | Gly | Tyr | Ser | Leu | Gly | Ala | His | Val | Ala | Gly |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Tyr | Ala | Gly | Asn | Phe | Val | Lys | Gly | Thr | Val | Gly | Arg | Ile | Thr | Gly | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Pro | Ala | Gly | Pro | Met | Phe | Glu | Gly | Ala | Asp | Ile | His | Lys | Arg | Leu |
| | | 195 | | | | 200 | | | | | 205 | | | | |
| Ser | Pro | Asp | Asp | Ala | Asp | Phe | Val | Asp | Val | Leu | His | Thr | Tyr | Thr | Arg |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Phe | Gly | Leu | Ser | Ile | Gly | Ile | Gln | Met | Pro | Val | Gly | His | Ile | Asp |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Ile | Tyr | Pro | Asn | Gly | Gly | Asp | Phe | Gln | Pro | Gly | Cys | Gly | Leu | Asn | Asp |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Val | Leu | Gly | Ser | Ile | Ala | Tyr | Gly | Thr | Ile | Thr | Glu | Val | Val | Lys | Cys |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Glu | His | Glu | Arg | Ala | Val | His | Leu | Phe | Val | Asp | Ser | Leu | Val | Asn | Gln |
| | | 275 | | | | 280 | | | | | 285 | | | | |
| Asp | Lys | Pro | Ser | Phe | Ala | Phe | Gln | Cys | Thr | Asp | Ser | Asn | Arg | Phe | Lys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Lys | Gly | Ile | Cys | Leu | Ser | Cys | Arg | Lys | Asn | Arg | Cys | Asn | Ser | Ile | Gly |
| 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| Tyr | Asn | Ala | Lys | Lys | Met | Arg | Asn | Lys | Arg | Asn | Ser | Lys | Met | Tyr | Leu |
| | | | 325 | | | | | 330 | | | | | 335 | | |
| Lys | Thr | Arg | Ala | Gly | Met | Pro | Phe | Arg | Val | Tyr | His | Tyr | Gln | Met | Lys |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ile | His | Val | Phe | Ser | Tyr | Lys | Asn | Met | Gly | Glu | Ile | Glu | Pro | Thr | Phe |
| | 355 | | | | | 360 | | | | | 365 | | | | |
| Tyr | Val | Thr | Leu | Tyr | Gly | Thr | Asn | Ala | Asp | Ser | Gln | Thr | Leu | Pro | Leu |
| | 370 | | | | | 375 | | | | | 380 | | | | |

Glu Ile Val Glu Arg Ile Glu Gln Asn Ala Thr Asn Thr Phe Leu Val

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 | | | | | 390 | | | | | 395 | | | | 400 |
| Tyr | Thr | Glu | Glu | Asp | Leu | Gly | Asp | Leu | Leu | Lys | Ile | Gln | Leu | Trp |
| | | | | 405 | | | | | 410 | | | | 415 | |
| Glu | Gly | Ala | Ser | Gln | Ser | Trp | Tyr | Asn | Leu | Trp | Lys | Glu | Phe | Ser |
| | | | 420 | | | | | 425 | | | | | 430 | |
| Tyr | Leu | Ser | Gln | Pro | Arg | Asn | Pro | Gly | Arg | Glu | Leu | Asn | Ile | Arg |
| | | 435 | | | | | 440 | | | | | 445 | | Arg |
| Ile | Arg | Val | Lys | Ser | Gly | Glu | Thr | Gln | Arg | Lys | Leu | Thr | Phe | Cys |
| | 450 | | | | | 455 | | | | 460 | | | | Thr |
| Glu | Asp | Pro | Glu | Asn | Thr | Ser | Ile | Ser | Pro | Gly | Arg | Glu | Leu | Trp |
| 465 | | | | | 470 | | | | | 475 | | | | 480 |
| Arg | Lys | Cys | Arg | Asp | Gly | Trp | Arg | Met | Lys | Asn | Glu | Thr | Ser | Pro |
| | | | | 485 | | | | | 490 | | | | | 495 |
| Val | Glu | Leu | Pro | | | | | | | | | | | |
| | | | 500 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1035 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AGC | AAC | TCC | GTT | CCT | CTG | CTC | TGT | TTC | TGG | AGC | CTC | TGC | TAT | TGC | 48 |
| Met | Ser | Asn | Ser | Val | Pro | Leu | Leu | Cys | Phe | Trp | Ser | Leu | Cys | Tyr | Cys | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| TTT | GCT | GCG | GGG | AGC | CCC | GTA | CCT | TTT | GGT | CCA | GAG | GGA | CGG | CTG | GAA | 96 |
| Phe | Ala | Ala | Gly | Ser | Pro | Val | Pro | Phe | Gly | Pro | Glu | Gly | Arg | Leu | Glu | |
| | | | 20 | | | | 25 | | | | | 30 | | | | |
| GAT | AAG | CTC | CAC | AAA | CCC | AAA | GCT | ACA | CAG | ACT | GAG | GTC | AAA | CCA | TCT | 144 |
| Asp | Lys | Leu | His | Lys | Pro | Lys | Ala | Thr | Gln | Thr | Glu | Val | Lys | Pro | Ser | |
| | | 35 | | | | 40 | | | | 45 | | | | | | |
| GTG | AGG | TTT | AAC | CTC | CGC | ACC | TCC | AAG | GAC | CCA | GAG | CAT | GAA | GGA | TGC | 192 |
| Val | Arg | Phe | Asn | Leu | Arg | Thr | Ser | Lys | Asp | Pro | Glu | His | Glu | Gly | Cys | |
| | 50 | | | | | 55 | | | | 60 | | | | | | |
| TAC | CTC | TCC | GTC | GGC | CAC | AGC | CAG | CCC | TTA | GAA | GAC | TGC | AGT | TTC | AAC | 240 |
| Tyr | Leu | Ser | Val | Gly | His | Ser | Gln | Pro | Leu | Glu | Asp | Cys | Ser | Phe | Asn | |
| 65 | | | | 70 | | | 75 | | | 80 | | | | | | |
| ATG | ACA | GCT | AAA | ACC | TTT | TTC | ATC | ATT | CAC | GGA | TGG | ACG | ATG | AGC | GGT | 288 |
| Met | Thr | Ala | Lys | Thr | Phe | Phe | Ile | Ile | His | Gly | Trp | Thr | Met | Ser | Gly | |
| | | | 85 | | | | 90 | | | | | | 95 | | | |
| ATC | TTT | GAA | AAC | TGG | CTG | CAC | AAA | CTC | GTG | TCA | GCC | CTG | CAC | ACA | AGA | 336 |
| Ile | Phe | Glu | Asn | Trp | Leu | His | Lys | Leu | Val | Ser | Ala | Leu | His | Thr | Arg | |
| | | | 100 | | | | 105 | | | | | 110 | | | | |
| GAG | AAA | GAC | GCC | AAT | GTA | GTT | GTG | GTT | GAC | TGG | CTC | CCC | CTG | GCC | CAC | 384 |
| Glu | Lys | Asp | Ala | Asn | Val | Val | Val | Val | Asp | Trp | Leu | Pro | Leu | Ala | His | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| CAG | CTT | TAC | ACG | GAT | GCG | GTC | AAT | AAT | ACC | AGG | GTG | GTG | GGA | CAC | AGC | 432 |
| Gln | Leu | Tyr | Thr | Asp | Ala | Val | Asn | Asn | Thr | Arg | Val | Val | Gly | His | Ser | |
| | 130 | | | | | 135 | | | | 140 | | | | | | |
| ATT | GCC | AGG | ATG | CTC | GAC | TGG | CTG | CAG | GAG | AAG | GAC | GAT | TTT | TCT | CTC | 480 |
| Ile | Ala | Arg | Met | Leu | Asp | Trp | Leu | Gln | Glu | Lys | Asp | Asp | Phe | Ser | Leu | |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 | |
| GGG | AAT | GTC | CAC | TTG | ATC | GGC | TAC | AGC | CTC | GGA | GCG | CAC | GTG | GCC | GGG | 528 |
| Gly | Asn | Val | His | Leu | Ile | Gly | Tyr | Ser | Leu | Gly | Ala | His | Val | Ala | Gly | |
| | | | 165 | | | | 170 | | | | | | 175 | | | |
| TAT | GCA | GGC | AAC | TTC | GTG | AAA | GGA | ACG | GTG | GGC | CGA | ATC | ACA | GGT | TTG | 576 |

Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
 180 185 190
 GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC AAG AGG CTC 624
 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
 195 200 205
 TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC TAC ACG CGT 672
 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
 210 215 220
 TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC CAC ATT GAC 720
 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
 225 230 235 240
 ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA CTC AAC GAT 768
 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
 245 250 255
 GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG GTA AAA TGT 816
 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
 260 265 270
 GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG GTG AAT CAG 864
 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
 275 280 285
 GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT CGC TTC AAA 912
 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
 290 295 300
 AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT AGC ATT GGC 960
 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
 305 310 315 320
 TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA ATG TAC CTA 1008
 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
 325 330 335
 AAA ACC CGG GCA GGC ATG CCT TTC AGA 1035
 Lys Thr Arg Ala Gly Met Pro Phe Arg
 340 345

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1 5 10 15
 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
 20 25 30
 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
 35 40 45
 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
 50 55 60
 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
 65 70 75 80
 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
 85 90 95
 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
 100 105 110
 Glu Lys Asp Ala Asn Val Val Val Asp Trp Leu Pro Leu Ala His
 115 120 125
 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
 130 135 140
 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
 145 150 155 160
 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly

Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
 165 170 175
 180 185 190
 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
 195 200 205
 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
 210 215 220
 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
 225 230 235 240
 Ile Tyr Pro Asn Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
 245 250 255
 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
 260 265 270
 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
 275 280 285
 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
 290 295 300
 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
 305 310 315 320
 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
 325 330 335
 Lys Thr Arg Ala Gly Met Pro Phe Arg
 340 345

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTG GGA TCC ATC GCC TAT GGC ACG ATC GCG GAG GTG GTG AAG TGC GAG 48
 Leu Gly Ser Ile Ala Tyr Gly Thr Ile Ala Glu Val Val Lys Cys Glu
 1 5 10 15
 CAT GAG CGG GCC GTG CAT CTC TTT GTG GAC TCC CTG GTG AAC CAG GAC 96
 His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln Asp
 20 25 30
 AAG CCG AGC TTT GCC TTC CAG TGC ACA GAC TCC AAC CGC TTC AAA AAA 144
 Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys Lys
 35 40 45
 GGG ATC TGT CTC AGC TGC CGG AAG AAC CGC TGT AAC GGC ATC GGC TAC 192
 Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Gly Ile Gly Tyr
 50 55 60
 AAT GCT AAG AAG ACG AGG AAT AAG AGG AAC ACC 225
 Asn Ala Lys Lys Thr Arg Asn Lys Arg Asn Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Gly Ser Ile Ala Tyr Gly Thr Ile Ala Glu Val Val Lys Cys Glu
 1 5 10 15
 His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln Asp

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | 20 | | | | | | 25 | | | | | 30 | | | | |
| Lys | Pro | Ser | Phe | Ala | Phe | Gln | Cys | Thr | Asp | Ser | Asn | Arg | Phe | Lys | Lys | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Gly | Ile | Cys | Leu | Ser | Cys | Arg | Lys | Asn | Arg | Cys | Asn | Gly | Ile | Gly | Tyr | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Asn | Ala | Lys | Lys | Thr | Arg | Asn | Lys | Arg | Asn | Thr | | | | | | | |
| 65 | | | | | 70 | | | | 75 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Glu | Ser | Lys | Ala | Leu | Leu | Val | Leu | Thr | Leu | Ala | Val | Trp | Leu | Gln | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Ser | Leu | Thr | Ala | Ser | Arg | Gly | Gly | Val | Ala | Ala | Ala | Asp | Gln | Arg | Arg | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Asp | Phe | Ile | Asp | Ile | Glu | Ser | Lys | Phe | Ala | Leu | Arg | Thr | Pro | Glu | Asp | | |
| | 35 | | | | | | 40 | | | | | 45 | | | | | |
| Thr | Ala | Glu | Asp | Thr | Cys | His | Leu | Ile | Pro | Gly | Val | Ala | Glu | Ser | Val | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Ala | Thr | Cys | His | Phe | Asn | His | Ser | Ser | Lys | Thr | Phe | Met | Val | Ile | His | | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | | |
| Gly | Trp | Thr | Val | Thr | Gly | Met | Tyr | Glu | Ser | Trp | Val | Pro | Lys | Leu | Val | | |
| | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Ala | Ala | Leu | Tyr | Lys | Arg | Glu | Pro | Asp | Ser | Asn | Val | Ile | Val | Val | Asp | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Trp | Leu | Ser | Arg | Ala | Gln | Glu | His | Tyr | Pro | Val | Ser | Ala | Gly | Tyr | Thr | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Lys | Leu | Val | Gly | Gln | Asp | Val | Ala | Arg | Phe | Ile | Asn | Trp | Met | Glu | Glu | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Glu | Phe | Asn | Tyr | Pro | Leu | Asp | Asn | Val | His | Leu | Leu | Gly | Tyr | Ser | Leu | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Gly | Ala | His | Ala | Ala | Gly | Ile | Ala | Gly | Ser | Leu | Thr | Asn | Lys | Lys | Val | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| Asn | Arg | Ile | Thr | Gly | Leu | Asp | Pro | Ala | Gly | Pro | Asn | Phe | Glu | Tyr | Ala | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| Glu | Ala | Pro | Ser | Arg | Leu | Ser | Pro | Asp | Asp | Ala | Asp | Phe | Val | Asp | Val | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Leu | His | Thr | Phe | Thr | Arg | Gly | Ser | Pro | Gly | Arg | Ser | Ile | Gly | Ile | Gln | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Lys | Pro | Val | Gly | His | Val | Asp | Ile | Tyr | Pro | Asn | Gly | Gly | Thr | Phe | Gln | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Pro | Gly | Cys | Asn | Ile | Gly | Glu | Ala | Ile | Arg | Val | Ile | Ala | Glu | Arg | Gly | | |
| | | | 245 | | | | | | 250 | | | | | 255 | | | |
| Leu | Gly | Asp | Val | Asp | Gln | Leu | Val | Lys | Cys | Ser | His | Glu | Arg | Ser | Ile | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | |
| His | Leu | Phe | Ile | Asp | Ser | Leu | Leu | Asn | Glu | Glu | Asn | Pro | Ser | Lys | Ala | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| Tyr | Arg | Cys | Ser | Ser | Lys | Glu | Ala | Phe | Glu | Lys | Gly | Leu | Cys | Leu | Ser | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| Cys | Arg | Lys | Asn | Arg | Cys | Asn | Asn | Leu | Gly | Tyr | Glu | Ile | Asn | Lys | Val | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| Arg | Ala | Lys | Arg | Ser | Ser | Lys | Met | Tyr | Leu | Lys | Thr | Arg | Ser | Gln | Met | | |
| | | | 325 | | | | | | 330 | | | | | 335 | | | |
| Pro | Tyr | Lys | Val | Phe | His | Tyr | Gln | Val | Lys | Ile | His | Phe | Ser | Gly | Thr | | |
| | | 340 | | | | | | 345 | | | | 350 | | | | | |
| Glu | Ser | Glu | Thr | His | Thr | Asn | Gln | Ala | Phe | Glu | Ile | Ser | Leu | Tyr | Gly | | |

7' cont.

71
cont.

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | | | | | | | | | | |
|------------|------------|-----|------------|----------|------------|------------|------------|------------|------------|------------|------------|------------|-----|-----------|-----|
| Met 1 | Asp | Thr | Ser | Pro 5 | Leu | Cys | Phe | Ser | Ile 10 | Leu | Leu | Val | Leu | Cys 15 | Ile |
| Phe | Ile | Gln | Ser 20 | Ser | Ala | Leu | Gly | Gln 25 | Ser | Leu | Lys | Pro 30 | Glu | Pro | Phe |
| Gly | Arg | Arg | Ala 35 | Gln | Ala | Val | Glu 40 | Thr | Asn | Lys | Thr 45 | Leu | His | Glu | Met |
| Lys | Thr 50 | Arg | Phe | Leu | Leu | Phe 55 | Gly | Glu | Thr | Asn 60 | Gln | Gly | Cys | Gln | Ile |
| Arg 65 | Ile | Asn | His | Pro | Asp 70 | Thr | Leu | Gln | Glu | Cys 75 | Gly | Phe | Asn | Ser | Ser |
| Leu | Pro | Leu | Val 85 | Met | Ile | Ile | His | Gly | Trp 90 | Ser | Val | Asp | Gly | Val | Leu |
| Glu | Asn | Trp | Ile 100 | Trp | Gln | Met | Val | Ala | Ala | Leu | Lys | Ser 110 | Gln | Pro | Ala |
| Gln | Pro | Val | Asn 115 | Val | Gly | Leu | Val | Asp 120 | Trp | Ile | Thr 125 | Leu | Ala | His | Asp |
| His | Tyr 130 | Thr | Ile | Ala | Val | Arg 135 | Asn | Thr | Arg | Leu 140 | Val | Gly | Lys | Glu | Val |
| Ala 145 | Ala | Leu | Leu | Arg | Trp 150 | Leu | Glu | Glu | Ser | Val 155 | Gln | Leu | Ser | Arg | Ser |
| His | Val | His | Leu 165 | Ile | Gly | Tyr | Ser | Leu | Gly | Ala 170 | His | Val | Ser | Gly | Phe |
| Ala | Gly | Ser | Ser 180 | Ile | Gly | Gly | Thr | His 185 | Lys | Ile | Gly | Arg 190 | Ile | Thr | Gly |
| Leu | Asp 195 | Ala | Ala | Gly | Pro | Leu | Phe 200 | Glu | Gly | Ser | Ala 205 | Pro | Ser | Asn | Arg |
| Leu | Ser 210 | Pro | Asp | Asp | Ala | Asn 215 | Phe | Val | Asp | Ala 220 | Ile | His | Thr | Phe | Thr |
| Arg 225 | Glu | His | Met | Gly | Leu 230 | Ser | Val | Gly | Ile | Lys 235 | Gln | Pro | Ile | Gly | His |
| Tyr | Asp | Phe | Tyr 245 | Pro | Asn | Gly | Gly | Ser | Phe 250 | Gln | Pro | Gly | Cys | His | Phe |
| Leu | Glu | Leu | Tyr 260 | Arg | His | Ile | Ala 265 | Gln | His | Gly | Phe 270 | Asn | Ala | Ile | Thr |
| Gln | Thr 275 | Ile | Lys | Cys | Ser | His 280 | Glu | Arg | Ser | Val | His 285 | Leu | Phe | Ile | Asp |
| Ser | Leu | Leu | His | Ala | Gly | Thr | Gln | Ser | Met | Ala | Tyr | Pro | Cys | Gly | Asp |

(2) INFORMATION FOR SEQ ID NO:15:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Pro Ala Glu Pro Cys Phe Gln Gly Thr Pro Glu Leu Val Arg Leu

[illegible]

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (v) FRAGMENT TYPE: internal

Gly Pro Glu Gly Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr
1 5 10 15
Cys

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (A) DESCRIPTION: /desc = "Oligonucleotide"

TTTTTTTTTT TGA

(2) INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
GATCAATCGC

10

(2) INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
TAGGACATGC ACAGTGTAACT CTG

23

71
cont.
(2) INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
GATTGTGCTG GCCACTTCTC

20

(2) INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
GACTCTCCAG GGACTGAAG

19

(2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 36
 (D) OTHER INFORMATION: /mod_base= i
 (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 37
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 41
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 47
 (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGNNGGG NNGGGNNG 48

(2) INFORMATION FOR SEQ ID NO:23:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
 CACACACAGG CCACGCGTCG ACTAGTAC 28

7'
 6' 5' 4' 3' 2' 1'

(2) INFORMATION FOR SEQ ID NO:24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
 ACCACCATGG AGAGCAAAGC CCTG 24

(2) INFORMATION FOR SEQ ID NO:25:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
 CCAGTTTCAG CCTGACTTCT TATTC 25

(2) INFORMATION FOR SEQ ID NO:26:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
GGCTGTGGAC TCAACGATGT C 21

(2) INFORMATION FOR SEQ ID NO:27:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
CCGGGTGGGT AGGTACATTT TG 22

(2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
GGGGGTGACT TCCAGCCAGG CTGTG 25

7' cord.
(2) INFORMATION FOR SEQ ID NO:29:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
AACTCTGAAA GGCATGCCTG CCCGG 25

(2) INFORMATION FOR SEQ ID NO:30:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
TGAAGGTCGG AGTCAACGGA TTTGGT 26

(2) INFORMATION FOR SEQ ID NO:31:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CATGTGGGCC ATGAGGTCCA CCAC 24